**GL-FP2.4.8.6. QTL-seq analysis for identification of genomic regions associated with days to flowering**

*Objective of activity and intended output:*

Identification of genomic region responsible for days to flowering through sequencing based BSA approach.

*Materials and methods:*

Days to fifty percent flowering is an important trait for development of early duration varieties.

Two parents ICP 5529 (late flowering-102 to 105 days) and ICP 11605 (early flowering-66 to 67 days) was selected for development of F2 mapping population. Based on phenotyping two extreme pools (early and late) was constructed. Sequencing data of two pools (Early flowering pools and Late flowering pool along with ICP 5529 was used for QTL-seq analysis

Results and interpretation:

A total of 17.95, 17.57 and 45.05 million reads were generated for Early flowering pools and Late flowering pool and ICP 5529, respectively. The generated data were ranged from 9.8 to 17.10 X coverage of the pigeonpea genome.

*Next Step:*

QTL-seq pipeline will be used to identify genomic regions for days to flowering.